

SEQUENCE LISTING

<110> Desgroseillers, Luc
Mouland, Andrew J.
Duchaine, Thomas J.
Luo, Ming J.
Wickham, Louise J.
Cohen, Eric A. J.

<120> Mammalian staufer and use thereof

<130> 12810.88

<150> US 09/316,048

<151> 1999-05-21

<160> 56

<170> PatentIn version 3.2

<210> 1

<211> 3506

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (409)..(2139)

<400> 1

acttctctgcc gggctgcggg cgcctgagcg ctcttcagcg tttgcgcggc ggctgcgcgt 60

ctctctcggc tcccgccttc tttgaccgac tccccccccc ggcccggcgg cgcccgcctc 120

ctccacgggc actccgcctc ttcctcctt tcgtcccttc ttctctccc ttttttctt 180

cttctctccc ctctcgccg ccaccgcca ggaccgccc cggggggacg agtccggagc 240

agcagccaga gtttattaac cacttaacct ctcagaactg aacaaagaca acattgttcc 300

tggaacgccc tcttttttaa aaaggtagaa ctttagactt catagcactg aattaacctg 360

cactgaaagc tgtttacctg catttggttca cttttgttga aagtgacc atg tct caa 417
Met Ser Gln
1

gtt caa gtg caa gtt cag aac cca tct gct gct ctc tca ggg agc caa 465
Val Gln Val Gln Val Gln Asn Pro Ser Ala Ala Leu Ser Gly Ser Gln
5 10 15

ata ctg aac aag aac cag tct ctt ctc tca cag cct ttg atg agt att 513
Ile Leu Asn Lys Asn Gln Ser Leu Leu Ser Gln Pro Leu Met Ser Ile
20 25 30 35

cct tct act act agc tct ctg ccc tct gaa aat gca ggt aga ccc att 561
Pro Ser Thr Thr Ser Ser Leu Pro Ser Glu Asn Ala Gly Arg Pro Ile
40 45 50

caa aac tct gct tta ccc tct gca tct att aca tcc acc agt gca gct 609
Gln Asn Ser Ala Leu Pro Ser Ala Ser Ile Thr Ser Thr Ser Ala Ala

55										60										65										
gca gaa agc ata acc cct act gta gaa cta aat gca ctg tgc atg aaa	Ala Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys Met Lys	657																												
70	75	80																												
ctt gga aaa aaa cca atg tat aag cct gtt gac cct tac tct cgg atg	Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser Arg Met	705																												
85	90	95																												
cag tcc acc tat aac tac aac atg aga gga ggt gct tat ccc ccg agg	Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro Pro Arg	753																												
100	105	110	115																											
tac ttt tac cca ttt cca gtt cca cct tta ctt tat caa gtg gaa ctt	Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val Glu Leu	801																												
120	125	130																												
tct gtg gga gga cag caa ttt aat ggc aaa gga aag aca aga cag gct	Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg Gln Ala	849																												
135	140	145																												
gcg aaa cac gat gct gct gcc aaa gcg ttg agg atc ctg cag aat gag	Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln Asn Glu	897																												
150	155	160																												
ccc ctg cca gag agg ctg gag gtg aat gga aga gaa tcc gaa gaa gaa	Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu Glu Glu	945																												
165	170	175																												
aat ctc aat aaa tct gaa ata agt caa gtg ttt gag att gca ctt aaa	Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala Leu Lys	993																												
180	185	190	195																											
cgg aac ttg cct gtg aat ttc gag gtg gcc cgg gag agt ggc cca ccc	Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly Pro Pro	1041																												
200	205	210																												
cac atg aag aac ttt gtg acc aag gtt tgc gtt ggg gag ttt gtg ggg	His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe Val Gly	1089																												
215	220	225																												
gaa ggt gaa ggg aaa agc aag aag att tca aag aaa aat gcc gcc ata	Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala Ile	1137																												
230	235	240																												
gct gtt ctt gag gag ctg aag aag tta ccg ccc ctg cct gca gtt gaa	Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala Val Glu	1185																												
245	250	255																												
cga gta aag cct aga atc aaa aag aaa aca aaa ccc ata gtc aag cca	Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val Lys Pro	1233																												
260	265	270	275																											
cag aca agc cca gaa tat ggc cag ggg atc aat ccg att agc cga ctg	Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser Arg Leu	1281																												
280	285	290																												
gcc cag atc cag cag gca aaa aag gag aag gag cca gag tac acg ctc	Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr Thr Leu	1329																												
295	300	305																												

ctc aca gag cga ggc ctc ccg cgc cgc agg gag ttt gtg atg cag gtg Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met Gln Val 310 315 320	1377
aag gtt gga aac cac act gca gaa gga acg ggc acc aac aag aag gtg Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys Lys Val 325 330 335	1425
gcc aag cgc aat gca gcc gag aac atg ctg gag atc ctt ggt ttc aaa Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly Phe Lys 340 345 350 355	1473
gtc ccg cag cgg cag ccc acc aaa ccc gca ctc aag tca gag gag aag Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu Glu Lys 360 365 370	1521
aca ccc ata aag aaa cca ggg gat gga aga aaa gta acc ttt ttt gaa Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe Phe Glu 375 380 385	1569
cct ggc tct ggg gat gaa aat ggg act agt aat aaa gag gat gag ttc Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp Glu Phe 390 395 400	1617
agg atg cct tat cta agt cat cag cag ctg cct gct gga att ctt ccc Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile Leu Pro 405 410 415	1665
atg gtg ccc gag gtc gcc cag gct gta gga gtt agt caa gga cat cac Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly His His 420 425 430 435	1713
acc aaa gat ttt acc agg gca gct ccg aat cct gcc aag gcc acg gta Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala Thr Val 440 445 450	1761
act gcc atg ata gcc cga gag ttg ttg tat ggg ggc acc tcg ccc aca Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser Pro Thr 455 460 465	1809
gcc gag acc att tta aag aat aac atc tct tca ggc cac gta ccc cat Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val Pro His 470 475 480	1857
gga cct ctc acg aga ccc tct gag caa ctg gac tat ctt tcc aga gtc Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser Arg Val 485 490 495	1905
cag gga ttc cag gtt gaa tac aaa gac ttc ccc aaa aac aac aag aac Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn Lys Asn 500 505 510 515	1953
gaa ttt gta tct ctt atc aat tgc tcc tct cag cca cct ctg atc agc Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu Ile Ser 520 525 530	2001
cat ggt atc ggc aag gat gtg gag tcc tgc cat gat atg gct gcg ctg His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala Ala Leu 535 540 545	2049

aac atc tta aag ttg ctg tct gag ttg gac caa caa agt aca gag atg	2097
Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr Glu Met	
550 555 560	
cca aga aca gga aac gga cca atg tct gtg tgt ggg agg tgc	2139
Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys	
565 570 575	
tgaacctttt ctggccatga accattataa aatcccaaca tatatactga aaatactgaa	2199
actgctttga aaatttgga tttctgatac ctccagtggg ccgagagaca cgggtgggtaa	2259
aggatgtggg cagcagcagg gaagacaaca gaaacacaag gaggcggctg tggccggctg	2319
gactgtgctg gggtttggtg tgatggccac tcggtgacct ggcggtcctt acgcaatagc	2379
agctgcctgt ggggaagaag ggctgcccag ccagctggtt ctcccgggac accagcagat	2439
ccacaccctg ggcacctccg tgtttggtct tttttttccc ctgtgtgaaa gaagaaacgg	2499
cacgacctt tctcaagctg gctcactcag acacattggg acaaaccctg gacagccatg	2559
ccagagagag gcctttgacc ggccccagag ctaaaagcac cagagaaaat caaatgcttc	2619
ctactcagcg tgaccaact tttctagtgt gccacggccc caccacctcc tgcagtaccc	2679
acaccatcac cactgctttc tcttccaaca gtgatctgta ttcttagttt cattattttc	2739
ttttgattga tatgacacta tataaaattt tcatttgaga atttctcaat tgtatctagt	2799
taaatagcac agtttgga aa cttgtctgag actgacttta tcaataatct aaccgacaaa	2859
gatcatatcc atgtgtatgt ggtagacat ttttatttca ttgactaacc caggacagtt	2919
tcagtgatgc aaattgtgtg ccctctgggt cagctgaaac agtcctggac tttcaaaaac	2979
cttgaataag tctccacag ttgtataaat tggacaattt aggaatttta aacttttagat	3039
gatcatttgg ttccattttt atttcatttt tatttttgtt aatgcaaaca ggacttaaat	3099
gaactttgat ctctgtttta aagattatta aaaaacattg tgtatctata catatggctc	3159
ttgaggactt agctttcact acactacagg atatgatctc catgtagtcc atataaacct	3219
gcagagtgat tttccagagt gctcgatact gttaattaca tctccattag ggctgaaaag	3279
aatgacctac gtttctgtat acagctgtgt tgcttttgat gttgtgttac tgtacacaga	3339
agtgtgtgca ctgaggctct gcgtgtggtc cgtatggaaa acctggtagc cctgcgagtt	3399
aagtactgct tccattcatt gtttacgctg gaatttttct ccccatggaa tgtaagtaaa	3459
acttaagtgt ttgtcatcaa taaatggtaa tactaaaaaa aaaaaaa	3506

<210> 2
 <211> 577
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ser Gln Val Gln Val Gln Val Gln Asn Pro Ser Ala Ala Leu Ser
1 5 10 15

Gly Ser Gln Ile Leu Asn Lys Asn Gln Ser Leu Leu Ser Gln Pro Leu
20 25 30

Met Ser Ile Pro Ser Thr Thr Ser Ser Leu Pro Ser Glu Asn Ala Gly
35 40 45

Arg Pro Ile Gln Asn Ser Ala Leu Pro Ser Ala Ser Ile Thr Ser Thr
50 55 60

Ser Ala Ala Ala Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu
65 70 75 80

Cys Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr
85 90 95

Ser Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr
100 105 110

Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln
115 120 125

Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr
130 135 140

Arg Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu
145 150 155 160

Gln Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser
165 170 175

Glu Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile
180 185 190

Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser
195 200 205

Gly Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu
210 215 220

Phe Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn
225 230 235 240

Ala Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro
245 250 255

Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile
260 265 270

Val Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile
275 280 285

Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu
290 295 300

Tyr Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val
305 310 315 320

Met Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn
325 330 335

Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu
340 345 350

Gly Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser
355 360 365

Glu Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr
370 375 380

Phe Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu
385 390 395 400

Asp Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly
405 410 415

Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln
420 425 430

Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys
435 440 445

Ala Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr
450 455 460

Ser Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His
465 470 475 480

Val Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu

485

490

495

Ser Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn
500 505 510

Asn Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro
515 520 525

Leu Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met
530 535 540

Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser
545 550 555 560

Thr Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg
565 570 575

Cys

<210> 3
<211> 3217
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (363)..(1850)

<400> 3
acttcctgcc. gggctgcggg cgctgagcg ctcttcagcg tttgcgcggc ggctgcgcgt 60
ctctctcggc tcccgcttc tttgaccgcc tcccccccc ggcccggcgg cgcccgctc 120
ctccacggcc actcgcctc ttccctccct tcgtcccttc ttctctccc ttttttcctt 180
cttccttccc ctctcgccg ccaccgcca ggaccgccg ccgggggacg agtccggagc 240
agcagccaga gtttattaac cacttaacct ctcagaactg aacaaagaca acattgttcc 300
tggaacgccc tctttttaaa aaagaaagca taaccctac tgtagaacta aatgcactgt 360
gc atg aaa ctt gga aaa aaa cca atg tat aag cct gtt gac cct tac 407
Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr
1 5 10 15
tct cgg atg cag tcc acc tat aac tac aac atg aga gga ggt gct tat 455
Ser Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr
20 25 30
ccc ccg agg tac ttt tac cca ttt cca gtt cca cct tta ctt tat caa 503
Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln
35 40 45

gtg gaa ctt tct gtg gga gga cag caa ttt aat ggc aaa gga aag aca	551
Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr	
50 55 60	
aga cag gct gcg aaa cac gat gct gct gcc aaa gcg ttg agg atc ctg	599
Arg Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu	
65 70 75	
cag aat gag ccc ctg cca gag agg ctg gag gtg aat gga aga gaa tcc	647
Gln Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser	
80 85 90 95	
gaa gaa gaa aat ctc aat aaa tct gaa ata agt caa gtg ttt gag att	695
Glu Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile	
100 105 110	
gca ctt aaa cgg aac ttg cct gtg aat ttc gag gtg gcc cgg gag agt	743
Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser	
115 120 125	
ggc cca ccc cac atg aag aac ttt gtg acc aag gtt tcg gtt ggg gag	791
Gly Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu	
130 135 140	
ttt gtg ggg gaa ggt gaa ggg aaa agc aag aag att tca aag aaa aat	839
Phe Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn	
145 150 155	
gcc gcc ata gct gtt ctt gag gag ctg aag aag tta ccg ccc ctg cct	887
Ala Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro	
160 165 170 175	
gca gtt gaa cga gta aag cct aga atc aaa aag aaa aca aaa ccc ata	935
Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile	
180 185 190	
gtc aag cca cag aca agc cca gaa tat ggc cag ggg atc aat ccg att	983
Val Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile	
195 200 205	
agc cga ctg gcc cag atc cag cag gca aaa aag gag aag gag cca gag	1031
Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu	
210 215 220	
tac acg ctc ctc aca gag cga ggc ctc ccg cgc cgc agg gag ttt gtg	1079
Tyr Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val	
225 230 235	
atg cag gtg aag gtt gga aac cac act gca gaa gga acg ggc acc aac	1127
Met Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn	
240 245 250 255	
aag aag gtg gcc aag cgc aat gca gcc gag aac atg ctg gag atc ctt	1175
Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu	
260 265 270	
ggc ttc aaa gtc ccg cag cgg cag ccc acc aaa ccc gca ctc aag tca	1223
Gly Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser	
275 280 285	

gag gag aag aca ccc ata aag aaa cca ggg gat gga aga aaa gta acc	1271
Glu Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr	
290 295 300	
ttt ttt gaa cct ggc tct ggg gat gaa aat ggg act agt aat aaa gag	1319
Phe Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu	
305 310 315	
gat gag ttc agg atg cct tat cta agt cat cag cag ctg cct gct gga	1367
Asp Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly	
320 325 330 335	
att ctt ccc atg gtg ccc gag gtc gcc cag gct gta gga gtt agt caa	1415
Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln	
340 345 350	
gga cat cac acc aaa gat ttt acc agg gca gct ccg aat cct gcc aag	1463
Gly His His Thr Lys Asp Phe Thr Thr Ala Ala Pro Asn Pro Ala Lys	
355 360 365	
gcc acg gta act gcc atg ata gcc cga gag ttg ttg tat ggg ggc acc	1511
Ala Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr	
370 375 380	
tcg ccc aca gcc gag acc att tta aag aat aac atc tct tca ggc cac	1559
Ser Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His	
385 390 395	
gta ccc cat gga cct ctg acg aga ccc tct gag caa ctg gac tat ctt	1607
Val Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu	
400 405 410 415	
tcc aga gtc cag gga ttc cag gtt gaa tac aaa gac ttc ccc aaa aac	1655
Ser Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn	
420 425 430	
aac aag aac gaa ttt gta tct ctt atc aat tgc tcc tct cag cca cct	1703
Asn Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro	
435 440 445	
ctg atc agc cat ggt atc ggc aag gat gtg gag tcc tgc cat gat atg	1751
Leu Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met	
450 455 460	
gct gcg ctg aac atc tta aag ttg ctg tct gag ttg gac caa caa agt	1799
Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser	
465 470 475	
aca gag atg cca aga aca gga aac gga cca atg tct gtg tgt ggg agg	1847
Thr Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg	
480 485 490 495	
tgc tgaacctttt ctggccatga accattataa aatcccaaca tatatactga	1900
Cys	
aaatactgaa actgctttga aaatttggaa tttctgatac ctccagtggg ccgagagaca	1960
cggtgggtaa aggatgtggg cagcagcagg gaagacaaca gaaacacaag gaggcggctg	2020
tggccgggctg gactgtgctg gggtttgttg tgatggccac tcggtgacct ggcgggtccct	2080

```

acgcaatagc agctgcctgt ggggaagaag ggctgcccag ccagctgggt ctcccgggac 2140
accagcagat ccacaccctg ggcacctccg tgtttggtct ttttttccc ctgtgtgaaa 2200
gaagaaacgg cacgaccctt tctcaagctg gctcactcag acacattggg acaaaccctg 2260
gacagccatg ccagagagag gcctttgacc ggccccagag ctaaaagcac cagagaaaat 2320
caaatgcttc ctactcagcg tgaccaact tttctagtgt gccacggccc caccacctcc 2380
tgcagtaccc acaccatcac cactgctttc tttccaaca gtgatctgta ttcttagttt 2440
cattattttc ttttgattga tatgacacta tataaaattt tcatttgaga atttctcaat 2500
tgtatctagt taaatagcac agtttgaaa cttgtctgag actgacttta tcaataatct 2560
aaccgacaaa gatcatatcc atgtgtatgt ggtagacat tttatttca ttgactaacc 2620
caggacagtt tcagtgatgc aaattgtgtg cctctgggtt cagctgaaac agtcctggac 2680
tttcaaaaac cttgaataag tctccacag ttgtataaat tggacaattt aggaatttta 2740
aacttttagat gatcatttgg ttccattttt atttcatttt tatttttggt aatgcaaaca 2800
ggacttaaat gaactttgat ctctgtttta aagattatta aaaaacattg tgtatctata 2860
catatggctc ttgaggactt agctttcact acactacagg atatgatctc catgtagtcc 2920
atataaacct gcagagtgat tttccagagt gctcgatact gttaattaca tctccattag 2980
ggctgaaaag aatgacctac gtttctgtat acagctgtgt tgcttttgat gttgtgttac 3040
tgtacacaga agtgtgtgca ctgaggctct gcgtgtggtc cgtatggaaa acctggtagc 3100
cctgcgagtt aagtactgct tccattcatt gtttacgctg gaatttttct ccccatggaa 3160
tgtaagtaaa acttaagtgt ttgtcatcaa taaatggtaa tactaaaaaa aaaaaaa 3217

```

```

<210> 4
<211> 496
<212> PRT
<213> Homo sapiens

<400> 4

```

```

Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser
1           5           10           15

```

```

Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro
          20           25           30

```

```

Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val
          35           40           45

```

```

Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg
          50           55           60

```

Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln
65 70 75 80

Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu
85 90 95

Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala
100 105 110

Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly
115 120 125

Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe
130 135 140

Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala
145 150 155 160

Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala
165 170 175

Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val
180 185 190

Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser
195 200 205

Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr
210 215 220

Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met
225 230 235 240

Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys
245 250 255

Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly
260 265 270

Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu
275 280 285

Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe
290 295 300

Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp
 305 310 315 320

Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile
 325 330 335

Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly
 340 345 350

His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala
 355 360 365

Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser
 370 375 380

Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val
 385 390 395 400

Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser
 405 410 415

Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn
 420 425 430

Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu
 435 440 445

Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala
 450 455 460

Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr
 465 470 475 480

Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys
 485 490 495

<210> 5
 <211> 3142
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (288)..(1775)

<400> 5
 acttcctgcc gggctgcggg cgcctgagcg ctcttcagcg tttgcgcggc ggctgcgcgt

ctctctcggc tcccgccttc tttagaccgcc tccccccccc ggcccggcgg cgcccgcctc	120
ctccacgggcc actccgcctc ttcctctcct tcgtcccttc ttcctctccc ttttttcctt	180
cttccttccc ctccctcgccg ccaccgcca ggaccgcccgg ccggggggacg agtccggagc	240
agcagccaga aagcataacc cctactgtag aactaaatgc actgtgc atg aaa ctt	296
	Met Lys Leu 1
gga aaa aaa cca atg tat aag cct gtt gac cct tac tct cgg atg cag	344
Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser Arg Met Gln	
5 10 15	
tcc acc tat aac tac aac atg aga gga ggt gct tat ccc ccg agg tac	392
Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro Pro Arg Tyr	
20 25 30 35	
ttt tac cca ttt cca gtt cca cct tta ctt tat caa gtg gaa ctt tct	440
Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val Glu Leu Ser	
40 45 50	
gtg gga gga cag caa ttt aat ggc aaa gga aag aca aga cag gct gcg	488
Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg Gln Ala Ala	
55 60 65	
aaa cac gat gct gct gcc aaa gcg ttg agg atc ctg cag aat gag ccc	536
Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu Gln Asn Glu Pro	
70 75 80	
ctg cca gag agg ctg gag gtg aat gga aga gaa tcc gaa gaa gaa aat	584
Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu Glu Glu Asn	
85 90 95	
ctc aat aaa tct gaa ata agt caa gtg ttt gag att gca ctt aaa cgg	632
Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala Leu Lys Arg	
100 105 110 115	
aac ttg cct gtg aat ttc gag gtg gcc cgg gag agt ggc cca ccc cac	680
Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly Pro Pro His	
120 125 130	
atg aag aac ttt gtg acc aag gtt tcg gtt ggg gag ttt gtg ggg gaa	728
Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe Val Gly Glu	
135 140 145	
ggt gaa ggg aaa agc aag aag att tca aag aaa aat gcc gcc ata gct	776
Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala Ile Ala	
150 155 160	
ggt ctt gag gag ctg aag aag tta ccg ccc ctg cct gca gtt gaa cga	824
Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala Val Glu Arg	
165 170 175	
gta aag cct aga atc aaa aag aaa aca aaa ccc ata gtc aag cca cag	872
Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val Lys Pro Gln	
180 185 190 195	
aca agc cca gaa tat ggc cag ggg atc aat ccg att agc cga ctg gcc	920
Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser Arg Leu Ala	

200										205					210					
cag	atc	cag	cag	gca	aaa	aag	gag	aag	gag	cca	gag	tac	acg	ctc	ctc	968				
Gln	Ile	Gln	Gln	Ala	Lys	Lys	Glu	Lys	Glu	Pro	Glu	Tyr	Thr	Leu	Leu					
215				220				225												
aca	gag	cga	ggc	ctc	ccg	cgc	cgc	agg	gag	ttt	gtg	atg	cag	gtg	aag	1016				
Thr	Glu	Arg	Gly	Leu	Pro	Arg	Arg	Arg	Glu	Phe	Val	Met	Gln	Val	Lys					
230			235			240														
gtt	gga	aac	cac	act	gca	gaa	gga	acg	ggc	acc	aac	aag	aag	gtg	gcc	1064				
Val	Gly	Asn	His	Thr	Ala	Glu	Gly	Thr	Gly	Thr	Asn	Lys	Lys	Val	Ala					
245			250			255														
aag	cgc	aat	gca	gcc	gag	aac	atg	ctg	gag	atc	ctt	ggg	ttc	aaa	gtc	1112				
Lys	Arg	Asn	Ala	Ala	Glu	Asn	Met	Leu	Glu	Ile	Leu	Gly	Phe	Lys	Val					
260		265		270		275														
ccg	cag	cgg	cag	ccc	acc	aaa	ccc	gca	ctc	aag	tca	gag	gag	aag	aca	1160				
Pro	Gln	Arg	Gln	Pro	Thr	Lys	Pro	Ala	Leu	Lys	Ser	Glu	Glu	Lys	Thr					
280				285				290												
ccc	ata	aag	aaa	cca	ggg	gat	gga	aga	aaa	gta	acc	ttt	ttt	gaa	cct	1208				
Pro	Ile	Lys	Lys	Pro	Gly	Asp	Gly	Arg	Lys	Val	Thr	Phe	Phe	Glu	Pro					
295			300			305														
ggc	tct	ggg	gat	gaa	aat	ggg	act	agt	aat	aaa	gag	gat	gag	ttc	agg	1256				
Gly	Ser	Gly	Asp	Glu	Asn	Gly	Thr	Ser	Asn	Lys	Glu	Asp	Glu	Phe	Arg					
310		315		320																
atg	cct	tat	cta	agt	cat	cag	cag	ctg	cct	gct	gga	att	ctt	ccc	atg	1304				
Met	Pro	Tyr	Leu	Ser	His	Gln	Gln	Leu	Pro	Ala	Gly	Ile	Leu	Pro	Met					
325		330		335																
gtg	ccc	gag	gtc	gcc	cag	gct	gta	gga	gtt	agt	caa	gga	cat	cac	acc	1352				
Val	Pro	Glu	Val	Ala	Gln	Ala	Val	Gly	Val	Ser	Gln	Gly	His	His	Thr					
340		345		350																
aaa	gat	ttt	acc	agg	gca	gct	ccg	aat	cct	gcc	aag	gcc	acg	gta	act	1400				
Lys	Asp	Phe	Thr	Arg	Ala	Ala	Pro	Asn	Pro	Ala	Lys	Ala	Thr	Val	Thr					
360				365				370												
gcc	atg	ata	gcc	cga	gag	ttg	ttg	tat	ggg	ggc	acc	tcg	ccc	aca	gcc	1448				
Ala	Met	Ile	Ala	Arg	Glu	Leu	Leu	Tyr	Gly	Gly	Thr	Ser	Pro	Thr	Ala					
375			380			385														
gag	acc	att	tta	aag	aat	aac	atc	tct	tca	ggc	cac	gta	ccc	cat	gga	1496				
Glu	Thr	Ile	Leu	Lys	Asn	Asn	Ile	Ser	Ser	Gly	His	Val	Pro	His	Gly					
390		395		400																
cct	ctc	acg	aga	ccc	tct	gag	caa	ctg	gac	tat	ctt	tcc	aga	gtc	cag	1544				
Pro	Leu	Thr	Arg	Pro	Ser	Glu	Gln	Leu	Asp	Tyr	Leu	Ser	Arg	Val	Gln					
405		410		415																
gga	ttc	cag	gtt	gaa	tac	aaa	gac	ttc	ccc	aaa	aac	aac	aag	aac	gaa	1592				
Gly	Phe	Gln	Val	Glu	Tyr	Lys	Asp	Phe	Pro	Lys	Asn	Asn	Lys	Asn	Glu					
420		425		430		435														
ttt	gta	tct	ctt	atc	aat	tgc	tcc	tct	cag	cca	cct	ctg	atc	agc	cat	1640				
Phe	Val	Ser	Leu	Ile	Asn	Cys	Ser	Ser	Gln	Pro	Pro	Leu	Ile	Ser	His					
440				445				450												

ggc atc ggc aag gat gtg gag tcc tgc cat gat atg gct gcg ctg aac	1688
Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala Ala Leu Asn	
455 460 465	
atc tta aag ttg ctg tct gag ttg gac caa caa agt aca gag atg cca	1736
Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr Glu Met Pro	
470 475 480	
aga aca gga aac gga cca atg tct gtg tgt ggg agg tgc tgaacctttt	1785
Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys	
485 490 495	
ctggccatga accattataa aatcccaaca tatatactga aaatactgaa actgctttga	1845
aaatttgga tttctgatac ctccagtggg ccgagagaca cgggtgggtaa aggatgtggg	1905
cagcagcagg gaagacaaca gaaacacaag gaggcggctg tggccggctg gactgtgctg	1965
gggtttgttg tgatggccac tcggtgacct ggcggtccct acgcaatagc agctgcctgt	2025
ggggaagaag ggctgccag ccagctgggt ctcccgggac accagcagat ccacaccctg	2085
ggcacctccg tgttttgtct tttttttccc ctgtgtgaaa gaagaaacgg cagcaccct	2145
tctcaagctg gctcactcag acacattggg acaaaccctg gacagccatg ccagagagag	2205
gcctttgacc ggccccagag ctaaaagcac cagagaaaat caaatgcttc ctactcagcg	2265
tgaccaact tttctagtgt gccacggccc caccacctcc tgcagtaccc acaccatcac	2325
cactgctttc tcttccaaca gtgatctgta ttcttagttt cattattttc ttttgattga	2385
tatgacacta tataaaattt tcatttgaga atttctcaat tgtatctagt taaatagcac	2445
agtttgga cttgtctgag actgacttta tcaataatct aaccgacaaa gatcatatcc	2505
atgtgtatgt ggtagacat ttttatttca ttgactaacc caggacagtt tcagtgatgc	2565
aaattgtgtg ccctctgggt cagctgaaac agtcctggac tttcaaaaac cttgaataag	2625
tctcccacag ttgtataaat tggacaattt aggaatttta aacttttagat gatcatttgg	2685
ttccattttt atttcatttt tatttttggt aatgcaaaca ggacttaaat gaactttgat	2745
ctctgtttta aagattatta aaaaacattg tgtatctata catatggctc ttgaggactt	2805
agctttcact aactacagg atatgatctc catgtagtcc atataaacct gcagagtgat	2865
ttccagagt gctcgatact gttaattaca tctccattag ggctgaaaag aatgacctac	2925
gtttctgtat acagctgtgt tgcttttgat gttgtgttac tgtaacacaga agtgtgtgca	2985
ctgaggctct gcgtgtggtc cgtatggaaa acctggtagc cctgcgagtt aagtactgct	3045
tccattcatt gtttacgctg gaatttttct ccccatggaa tgtaagtaaa acttaagtgt	3105
ttgtcatcaa taaatggtaa tactaaaaaa aaaaaaa	3142

<211> 3348
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (494) .. (1981)

<400> 6
 acttcctgcc gggctgcggg cgctgagcg ctcttcagcg tttgcgcggc ggctgcgcgt 60
 ctctctcggc tcccgtttcc tttgaccgcc tccccccccc ggcccggcgg cgcccgcctc 120
 ctccacggcc actcgcctc ttccctccct tcgtcccttc ttctctccc ttttttcctt 180
 cttccttccc ctctcgcgg ccaccgcca ggaccgccgg ccgggggacg agtccggagc 240
 agcagccagc agcagccagg tggagttttg ctcttgtcgc ccaggctgga gtgcagtggc 300
 gtgatctcgg ctactgcaa cctccacctc ccaggtcagc gattttccca cttcagcctc 360
 ccgataagct gagattacag agtttattaa ccacttaacc ttcagaact gaacaaagac 420
 aacattgttc ctggaacgcc ctcttttttaaaaagaaagc ataacccta ctgtagaact 480
 aaatgcactg tgc atg aaa ctt gga aaa aaa cca atg tat aag cct gtt 529
 Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val
 1 5 10
 gac cct tac tct cgg atg cag tcc acc tat aac tac aac atg aga gga 577
 Asp Pro Tyr Ser Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly
 15 20 25
 ggt gct tat ccc ccg agg tac ttt tac cca ttt cca gtt cca cct tta 625
 Gly Ala Tyr Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu
 30 35 40
 ctt tat caa gtg gaa ctt tct gtg gga gga cag caa ttt aat ggc aaa 673
 Leu Tyr Gln Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys
 45 50 55 60
 gga aag aca aga cag gct gcg aaa cac gat gct gct gcc aaa gcg ttg 721
 Gly Lys Thr Arg Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu
 65 70 75
 agg atc ctg cag aat gag ccc ctg cca gag agg ctg gag gtg aat gga 769
 Arg Ile Leu Gln Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly
 80 85 90
 aga gaa tcc gaa gaa gaa aat ctc aat aaa tct gaa ata agt caa gtg 817
 Arg Glu Ser Glu Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val
 95 100 105
 ttt gag att gca ctt aaa cgg aac ttg cct gtg aat ttc gag gtg gcc 865
 Phe Glu Ile Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala
 110 115 120
 cgg gag agt ggc cca ccc cac atg aag aac ttt gtg acc aag gtt tcg 913
 Arg Glu Ser Gly Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser
 125 130 135 140

gtt ggg gag ttt gtg ggg gaa ggt gaa ggg aaa agc aag aag att tca	961
Val Gly Glu Phe Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser	
145 150 155	
aag aaa aat gcc gcc ata gct gtt ctt gag gag ctg aag aag tta ccg	1009
Lys Lys Asn Ala Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro	
160 165 170	
ccc ctg cct gca gtt gaa cga gta aag cct aga atc aaa aag aaa aca	1057
Pro Leu Pro Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr	
175 180 185	
aaa ccc ata gtc aag cca cag aca agc cca gaa tat ggc cag ggg atc	1105
Lys Pro Ile Val Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile	
190 195 200	
aat ccg att agc cga ctg gcc cag atc cag cag gca aaa aag gag aag	1153
Asn Pro Ile Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys	
205 210 215 220	
gag cca gag tac acg ctc ctc aca gag cga ggc ctc ccg cgc cgc agg	1201
Glu Pro Glu Tyr Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg	
225 230 235	
gag ttt gtg atg cag gtg aag gtt gga aac cac act gca gaa gga acg	1249
Glu Phe Val Met Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr	
240 245 250	
ggc acc aac aag aag gtg gcc aag cgc aat gca gcc gag aac atg ctg	1297
Gly Thr Asn Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu	
255 260 265	
gag atc ctt ggt ttc aaa gtc ccg cag cgg cag ccc acc aaa ccc gca	1345
Glu Ile Leu Gly Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala	
270 275 280	
ctc aag tca gag gag aag aca ccc ata aag aaa cca ggg gat gga aga	1393
Leu Lys Ser Glu Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg	
285 290 295 300	
aaa gta acc ttt ttt gaa cct ggc tct ggg gat gaa aat ggg act agt	1441
Lys Val Thr Phe Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser	
305 310 315	
aat aaa gag gat gag ttc agg atg cct tat cta agt cat cag cag ctg	1489
Asn Lys Glu Asp Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu	
320 325 330	
cct gct gga att ctt ccc atg gtg ccc gag gtc gcc cag gct gta gga	1537
Pro Ala Gly Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly	
335 340 345	
gtt agt caa gga cat cac acc aaa gat ttt acc agg gca gct ccg aat	1585
Val Ser Gln Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn	
350 355 360	
cct gcc aag gcc acg gta act gcc atg ata gcc cga gag ttg ttg tat	1633
Pro Ala Lys Ala Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr	
365 370 375 380	

ggg ggc acc tcg ccc aca gcc gag acc att tta aag aat aac atc tct Gly Gly Thr Ser Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser 385 390 395	1681
tca ggc cac gta ccc cat gga cct ctc acg aga ccc tct gag caa ctg Ser Gly His Val Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu 400 405 410	1729
gac tat ctt tcc aga gtc cag gga ttc cag gtt gaa tac aaa gac ttc Asp Tyr Leu Ser Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe 415 420 425	1777
ccc aaa aac aac aag aac gaa ttt gta tct ctt atc aat tgc tcc tct Pro Lys Asn Asn Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser 430 435 440	1825
cag cca cct ctg atc agc cat ggt atc ggc aag gat gtg gag tcc tgc Gln Pro Pro Leu Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys 445 450 455 460	1873
cat gat atg gct gcg ctg aac atc tta aag ttg ctg tct gag ttg gac His Asp Met Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp 465 470 475	1921
caa caa agt aca gag atg cca aga aca gga aac gga cca atg tct gtg Gln Gln Ser Thr Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val 480 485 490	1969
tgt ggg agg tgc tgaacctttt ctggccatga accattataa aatcccaaca Cys Gly Arg Cys 495	2021
tatatactga aaatactgaa actgctttga aaatttgga tttctgatac ctccagtggg	2081
ccgagagaca cgggtgggtaa aggatgtggg cagcagcagg gaagacaaca gaaacacaag	2141
gaggcggtctg tggccggctg gactgtgctg gggtttggtg tgatggccac tgggtgacct	2201
ggcggtccct acgcaatagc agctgcctgt ggggaagaag ggctgcccag ccagctgggt	2261
ctcccgggac accagcagat ccacaccctg ggcacctcg tgtttggtct tttttttccc	2321
ctgtgtgaaa gaagaaacgg cagaccct tctcaagctg gctcactcag acacattggg	2381
acaaaccctg gacagccatg ccagagagag gcctttgacc ggcccagag ctaaaagcac	2441
cagagaaaat caaatgcttc ctactcagcg tgacccaact tttctagtgt gccacggccc	2501
caccacctcc tgcagtaccc acaccatcac cactgctttc tcttccaaca gtgatctgta	2561
ttcttagttt cattattttc ttttgattga tatgacacta tataaaattt tcatttgaga	2621
atttctcaat tgtatctagt taaatagcac agtttgga cttgtctgag actgacttta	2681
tcaataatct aaccgacaaa gatcatatcc atgtgtatgt ggtagacat ttttatttca	2741
ttgactaacc caggacagtt tcagtgatgc aaattgtgtg ccctctgggt cagctgaaac	2801
agtcctggac tttcaaaaac cttgaataag tctcccacag ttgtataaat tggacaattt	2861
aggaatttta aacttttagat gatcatttgg ttccattttt atttcatttt tatttttggt	2921

aatgcaaaca ggactttaat gaactttgat ctctgtttta aagattatta aaaaacattg 2981
tgtatctata catatggctc ttgaggactt agctttcact acactacagg atatgatctc 3041
catgtagtcc atataaacct gcagagtgat tttccagagt gctcgatact gttaattaca 3101
tctccattag ggctgaaaag aatgacctac gtttctgtat acagctgtgt tgcttttgat 3161
gttgtgttac tgtacacaga agtgtgtgca ctgaggctct gcgtgtgggc cgtatggaaa 3221
acctggtagc cctgcgagtt aagtactgct tccattcatt gtttacgctg gaatttttct 3281
cccatggaa tgtaagtaaa acttaagtgt ttgtcatcaa taaatggtaa tactaaaaaa 3341
aaaaaaa 3348

<210> 7
<211> 2857
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (324)..(1784)

<400> 7
cgggcgcggc ccctcccccg tcacttcctg ccaggctgcg ggccccgagc cgctcttcag 60
cgtttgcgct ggctgtcgtc gcgtctgtgt gcgctcccc ttcttctgag ccccggcctg 120
ggggcgcccc ccttcgcctc cgccactcgc cctcttcctt cctctggctg gccccttttt 180
cctcgccgtc ttcacttget tcttcacctc ctgcgcgcgc cccaagaccg ccggcccccg 240
gacgagctct ggggaagcag ccagaaagta tagctttctac cattgagctc aatgcactgt 300
gtgtgaaact ggaaagaaaa cca atg tat aag ccc gtg gac cct cac tct cgg 353
Met Tyr Lys Pro Val Asp Pro His Ser Arg
1 5 10

atg cag tcc acc tac agc tat ggc atg cgt gga ggt gcc tat ccc ccc 401
Met Gln Ser Thr Tyr Ser Tyr Gly Met Arg Gly Gly Ala Tyr Pro Pro
15 20 25

aga tac ttt tac cca ttt cca gtc cca cct tta ctc tac caa gtt gag 449
Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val Glu
30 35 40

ctc tcc gtg ggc gga cag cag ttt aat ggg aaa gga aag atg aga cca 497
Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Met Arg Pro
45 50 55

ccc gtg aaa cac gat gcc cct gcc cgt gcg ctg agg act ctg cag agt 545
Pro Val Lys His Asp Ala Pro Ala Arg Ala Leu Arg Thr Leu Gln Ser
60 65 70

gaa ccc ctg cca gaa agg ttg gag gta aat gga aga gaa gca gag gaa 593
Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ala Glu Glu

75	80	85	90	
gaa aac ctc aat aaa tcg gaa ata agc caa gtg ttt gaa att gcg ctg				641
Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala Leu				
95		100	105	
aag cgg aat ttg cct gtg aat ttt gag gtg gcc cgg gag agt ggc cca				689
Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly Pro				
110		115	120	
cca cac atg aag aac ttt gtg acc agg gtt tca gtt ggg gaa ttt gta				737
Pro His Met Lys Asn Phe Val Thr Arg Val Ser Val Gly Glu Phe Val				
125		130	135	
ggg gaa gga gaa ggg aaa agc aag aag atc tcc aag aag aat gcg gcc				785
Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala				
140		145	150	
agg gct gtt ctg gag cag ctt agg agg ctg cca ccc ctc cct gct gtg				833
Arg Ala Val Leu Glu Gln Leu Arg Arg Leu Pro Pro Leu Pro Ala Val				
155		160	165	170
gag cga gtg aag ccc aga atc aag aag aaa agt cag ccc acc tgc aag				881
Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Ser Gln Pro Thr Cys Lys				
175		180	185	
aca gcc ccg gat tat ggc caa ggg atg aat cct att agt aga ctt gca				929
Thr Ala Pro Asp Tyr Gly Gln Gly Met Asn Pro Ile Ser Arg Leu Ala				
190		195	200	
cag atc cag cag gca aaa aag gag aag gag cca gag tac atg ctc ctt				977
Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr Met Leu Leu				
205		210	215	
aca gaa cga ggt ctt cca cgt cgc agg gag ttt gtg atg cag gta aag				1025
Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val Met Gln Val Lys				
220		225	230	
gtt ggg cat cac act gca gaa gga gtg ggt acc aat aag aag gtg gcc				1073
Val Gly His His Thr Ala Glu Gly Val Gly Thr Asn Lys Lys Val Ala				
235		240	245	250
aag cgt aat gct gct gag aac atg ctg gag atc ctg ggg ttc aaa gtt				1121
Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly Phe Lys Val				
255		260	265	
ccc cag gcg cag cct gcc aag cca gca ctc aaa tca gaa gag aag act				1169
Pro Gln Ala Gln Pro Ala Lys Pro Ala Leu Lys Ser Glu Glu Lys Thr				
270		275	280	
cca gta aag aaa cca gga gac gga agg aaa gta acg ttt ttt gaa cct				1217
Pro Val Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe Phe Glu Pro				
285		290	295	
agc cct ggg gat gaa aat gga act agt aac aag gac gag gag ttc agg				1265
Ser Pro Gly Asp Glu Asn Gly Thr Ser Asn Lys Asp Glu Glu Phe Arg				
300		305	310	
atg cct tat ctt agc cat cag cag ctg cca gct gga att ctc ccc atg				1313
Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile Leu Pro Met				
315		320	325	330

gtg ccg gaa gtt gcc cag gct gtc ggg gtt agt caa gga cac cac acc	1361
Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly His His Thr	
335 340 345	
aaa gat ttc acc agg gca gct cca aat cct gcc aag gca acg gta act	1409
Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala Thr Val Thr	
350 355 360	
gcc atg ata gcc cga gag ttg ttg tac ggg ggc acc tcg ccc aca gcc	1457
Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser Pro Thr Ala	
365 370 375	
gag acc att tta aag agt aac atc tct tca ggc cac gta ccc cat gga	1505
Glu Thr Ile Leu Lys Ser Asn Ile Ser Ser Gly His Val Pro His Gly	
380 385 390	
cct cgc act aga ccc tct gag caa ctg tac tac ctt tcc aga gcc cag	1553
Pro Arg Thr Arg Pro Ser Glu Gln Leu Tyr Tyr Leu Ser Arg Ala Gln	
395 400 405 410	
gga ttc cag gtt gaa tac aaa gat ttt ccc aag aac aac aag aac gag	1601
Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn Lys Asn Glu	
415 420 425	
tgt gta tct ctc atc aac tgc tcc tca cag ccg cct ctc gtc agt cat	1649
Cys Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu Val Ser His	
430 435 440	
ggc atc ggc aag gat gtg gag tcc tgt cat gat atg gct gca ctg aac	1697
Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala Ala Leu Asn	
445 450 455	
att tta aag ctg ctg tct gag ttg gac caa cag agc aca gag atg cca	1745
Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr Glu Met Pro	
460 465 470	
aga aca gga aat gga cca gtt tca gcg tgc ggg agg tgc tgaacctttt	1794
Arg Thr Gly Asn Gly Pro Val Ser Ala Cys Gly Arg Cys	
475 480 485	
ctggccacaa accattataa aaccaacat atatactgaa aatactgaga actgctttga	1854
aaatttgga tatctgataa ctccagtggg ccaagacatg gtggataaaa atgtggcaaa	1914
gacgacaaga aacttcaggt ggtagccctg gttgtgctgg cggctagtga tgatgctgtg	1974
ctctgccatc catccagaca gaaaccagcc ccaacgcctc cagttctgtt tttgcatcgt	2034
gacaaagaga gcacagccaa ttctcatgct ggcttcttca gatactttga aaaaccggga	2094
cagccacacc agagaggcct tatagcggcc ccggagctaa acggaccaga gaaaaggcca	2154
gtgcttccta ctgcacatga ctgactcagc tccgccacac gtagcaccac tgtaaccact	2214
gctttctctt cagtttcatt ttttctctt gattgatata acactataat tttcatttca	2274
gttccttagt cgtgtctact tacctagcag tttagaaact gtcagtcatg taactggcaa	2334
ggatcacagc ccggttggtt ggcattctgt gcctctggct tggctgaaca gttctggaat	2394

taccaccaga atccttgact cccctgcccct tgtataaatt ggacagctta ggacttttaa 2454
 acttttagatc aaaagatatg gtccttttta actttatttt taaggagcag actttaaaat 2514
 gagccctgac ctttaccat tataacagaa tttgtcaaaa ggagtgtttc ttgaggaggt 2574
 agcttttttt taccacacta caggacatta cctgtaggcc cagaagacta caggctggtg 2634
 tccctagagg gcccaatata gtcaattcca acctctaagt cggggaaagg tgacagggtt 2694
 cctggtgctg gtgtgcacag gggcaggcag gtcagctggc ctggggaaga gcattgtggc 2754
 tcctagtga gccctgttc cactcttggg ttagctggaa ccttcccact catggaatat 2814
 aagtaaactc actttctttg tcaccaataa atggtaatat taa 2857

<210> 8
 <211> 487
 <212> PRT
 <213> Mus musculus

<400> 8

Met Tyr Lys Pro Val Asp Pro His Ser Arg Met Gln Ser Thr Tyr Ser
 1 5 10 15

Tyr Gly Met Arg Gly Gly Ala Tyr Pro Pro Arg Tyr Phe Tyr Pro Phe
 20 25 30

Pro Val Pro Pro Leu Leu Tyr Gln Val Glu Leu Ser Val Gly Gly Gln
 35 40 45

Gln Phe Asn Gly Lys Gly Lys Met Arg Pro Pro Val Lys His Asp Ala
 50 55 60

Pro Ala Arg Ala Leu Arg Thr Leu Gln Ser Glu Pro Leu Pro Glu Arg
 65 70 75 80

Leu Glu Val Asn Gly Arg Glu Ala Glu Glu Glu Asn Leu Asn Lys Ser
 85 90 95

Glu Ile Ser Gln Val Phe Glu Ile Ala Leu Lys Arg Asn Leu Pro Val
 100 105 110

Asn Phe Glu Val Ala Arg Glu Ser Gly Pro Pro His Met Lys Asn Phe
 115 120 125

Val Thr Arg Val Ser Val Gly Glu Phe Val Gly Glu Gly Glu Gly Lys
 130 135 140

Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala Arg Ala Val Leu Glu Gln

145		150		155		160
Leu Arg Arg Leu	Pro Pro Leu Pro	Ala Val Glu Arg Val	Lys Pro Arg			
	165	170	175			
Ile Lys Lys Lys	Ser Gln Pro Thr	Cys Lys Thr Ala Pro	Asp Tyr Gly			
	180	185	190			
Gln Gly Met Asn	Pro Ile Ser Arg	Leu Ala Gln Ile	Gln Gln Ala Lys			
	195	200	205			
Lys Glu Lys Glu	Pro Glu Tyr Met	Leu Leu Thr Glu	Arg Gly Leu Pro			
	210	215	220			
Arg Arg Arg Glu	Phe Val Met Gln	Val Lys Val Gly	His His Thr Ala			
	225	230	235			240
Glu Gly Val Gly	Thr Asn Lys Lys	Val Ala Lys Arg	Asn Ala Ala Glu			
	245	250	255			
Asn Met Leu Glu	Ile Leu Gly Phe	Lys Val Pro Gln	Ala Gln Pro Ala			
	260	265	270			
Lys Pro Ala Leu	Lys Ser Glu Glu	Lys Thr Pro Val	Lys Lys Pro Gly			
	275	280	285			
Asp Gly Arg Lys	Val Thr Phe Phe	Glu Pro Ser Pro	Gly Asp Glu Asn			
	290	295	300			
Gly Thr Ser Asn	Lys Asp Glu Glu	Phe Arg Met Pro	Tyr Leu Ser His			
	305	310	315			320
Gln Gln Leu Pro	Ala Gly Ile Leu	Pro Met Val Pro	Glu Val Ala Gln			
	325	330	335			
Ala Val Gly Val	Ser Gln Gly His	His Thr Lys Asp	Phe Thr Arg Ala			
	340	345	350			
Ala Pro Asn Pro	Ala Lys Ala Thr	Val Thr Ala Met	Ile Ala Arg Glu			
	355	360	365			
Leu Leu Tyr Gly	Gly Thr Ser Pro	Thr Ala Glu Thr	Ile Leu Lys Ser			
	370	375	380			
Asn Ile Ser Ser	Gly His Val Pro	His Gly Pro Arg	Thr Arg Pro Ser			
	385	390	395			400

Glu Gln Leu Tyr Tyr Leu Ser Arg Ala Gln Gly Phe Gln Val Glu Tyr
405 410 415

Lys Asp Phe Pro Lys Asn Asn Lys Asn Glu Cys Val Ser Leu Ile Asn
420 425 430

Cys Ser Ser Gln Pro Pro Leu Val Ser His Gly Ile Gly Lys Asp Val
435 440 445

Glu Ser Cys His Asp Met Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser
450 455 460

Glu Leu Asp Gln Gln Ser Thr Glu Met Pro Arg Thr Gly Asn Gly Pro
465 470 475 480

Val Ser Ala Cys Gly Arg Cys
485

<210> 9

<211> 1026

<212> PRT

<213> Drosophila melanogaster

<400> 9

Met Gln His Asn Val His Ala Ala Arg Pro Ala Pro His Ile Arg Ala
1 5 10 15

Ala His His His Ser His Ser His Ala His Met His Leu His Pro Gly
20 25 30

Met Glu Gln His Leu Gly Pro Ser Leu Gln Gln Gln Gln Gln Pro Pro
35 40 45

Pro Pro Pro Gln Gln Pro Pro His Arg Asp Leu His Ala Arg Leu Asn
50 55 60

His His His Leu His Ala Gln Gln Gln Gln Gln Gln Gln Thr Ser Ser
65 70 75 80

Asn Gln Ala Ala Ala Val Ala Ala Ala Gly Ala Ala Tyr His His Gly
85 90 95

Asn Ile Asn Ser Asn Ser Gly Ser Asn Ile Ser Ser Asn Ser Asn Gln
100 105 110

Met Gln Lys Ile Arg Gln Gln His Gln His Leu Ser Ser Ser Asn Gly
115 120 125

Leu Leu Gly Asn Gln Pro Pro Gly Pro Pro Pro Gln Ala Phe Asn Pro
130 135 140

Leu Ala Gly Asn Pro Ala Ala Leu Ala Tyr Asn Gln Leu Pro Pro His
145 150 155 160

Pro Pro His His Met Ala Ala His Leu Gly Ser Tyr Ala Ala Pro Pro
165 170 175

Pro His Tyr Tyr Met Ser Gln Ala Lys Pro Ala Lys Tyr Asn His Tyr
180 185 190

Gly Ser Asn Ala Asn Ser Asn Ser Gly Ser Asn Asn Ser Asn Ser Asn
195 200 205

Tyr Ala Pro Lys Ala Ile Leu Gln Asn Thr Tyr Arg Asn Gln Lys Val
210 215 220

Val Val Pro Pro Val Val Gln Glu Val Thr Pro Val Pro Glu Pro Pro
225 230 235 240

Val Thr Thr Asn Asn Ala Thr Thr Asn Ser Thr Ser Asn Ser Thr Val
245 250 255

Ile Ala Ser Glu Pro Val Thr Gln Glu Asp Thr Ser Gln Lys Pro Glu
260 265 270

Thr Arg Gln Glu Pro Ala Ser Ala Asp Asp His Val Ser Thr Gly Asn
275 280 285

Ile Asp Ala Thr Gly Ala Leu Ser Asn Glu Asp Thr Ser Ser Ser Gly
290 295 300

Arg Gly Gly Lys Asp Lys Thr Pro Met Cys Leu Val Asn Glu Leu Ala
305 310 315 320

Arg Tyr Asn Lys Ile Thr His Gln Tyr Arg Leu Thr Glu Glu Arg Gly
325 330 335

Pro Ala His Cys Lys Thr Phe Thr Val Thr Leu Met Leu Gly Asp Glu
340 345 350

Glu Tyr Ser Ala Asp Gly Phe Lys Ile Lys Lys Ala Gln His Leu Ala

355

360

365

Ala Ser Lys Ala Ile Glu Glu Thr Met Tyr Lys His Pro Pro Pro Lys
 370 375 380

Ile Arg Arg Ser Glu Glu Gly Gly Pro Met Arg Thr His Ile Thr Pro
 385 390 395 400

Thr Val Glu Leu Asn Ala Leu Ala Met Lys Leu Gly Gln Arg Thr Phe
 405 410 415

Tyr Leu Leu Asp Pro Thr Gln Ile Pro Pro Thr Asp Ser Ile Val Pro
 420 425 430

Pro Glu Phe Ala Gly Gly His Leu Leu Thr Ala Pro Gly Pro Gly Met
 435 440 445

Pro Gln Pro Pro Pro Pro Pro Ala Tyr Ala Leu Arg Gln Arg Leu Gly
 450 455 460

Asn Gly Phe Val Pro Ile Pro Ser Gln Pro Met His Pro His Phe Phe
 465 470 475 480

His Gly Pro Gly Gln Arg Pro Phe Pro Pro Lys Phe Pro Ser Arg Phe
 485 490 495

Ala Leu Pro Pro Pro Leu Gly Ala His Val His His Gly Pro Asn Gly
 500 505 510

Pro Phe Pro Ser Val Pro Thr Pro Pro Ser Lys Ile Thr Leu Phe Val
 515 520 525

Gly Lys Gln Lys Phe Val Gly Ile Gly Arg Thr Leu Gln Gln Ala Lys
 530 535 540

His Asp Ala Ala Ala Arg Ala Leu Gln Val Leu Lys Thr Gln Ala Ile
 545 550 555 560

Ser Ala Ser Glu Glu Ala Leu Glu Asp Ser Met Asp Glu Gly Asp Lys
 565 570 575

Lys Ser Pro Ile Ser Gln Val His Glu Ile Gly Ile Lys Arg Asn Met
 580 585 590

Thr Val His Phe Lys Val Leu Arg Glu Glu Gly Pro Ala His Met Lys
 595 600 605

Asn Phe Ile Thr Ala Cys Ile Val Gly Ser Ile Val Thr Glu Gly Glu
610 615 620

Gly Asn Gly Lys Lys Val Ser Lys Lys Arg Ala Ala Glu Lys Met Leu
625 630 635 640

Val Glu Leu Gln Lys Leu Pro Pro Leu Thr Pro Thr Lys Gln Thr Pro
645 650 655

Leu Lys Arg Ile Lys Val Lys Thr Pro Gly Lys Ser Gly Ala Ala Ala
660 665 670

Arg Glu Gly Ser Val Val Ser Gly Thr Asp Gly Thr Met Gln Thr Gly
675 680 685

Lys Pro Glu Arg Arg Lys Arg Leu Asn Pro Pro Lys Asp Lys Leu Ile
690 695 700

Asp Met Asp Asp Ala Asp Asn Pro Ile Thr Lys Leu Ile Gln Leu Gln
705 710 715 720

Gln Thr Arg Lys Glu Lys Glu Pro Ile Phe Glu Leu Ile Ala Lys Asn
725 730 735

Gly Asn Glu Thr Ala Arg Arg Arg Glu Phe Val Met Glu Val Ser Ala
740 745 750

Ser Gly Ser Thr Ala Arg Gly Thr Gly Asn Ser Lys Lys Leu Ala Lys
755 760 765

Arg Asn Ala Ala Gln Ala Leu Phe Glu Leu Leu Glu Ala Val Gln Val
770 775 780

Thr Pro Thr Asn Glu Thr Gln Ser Ser Glu Glu Cys Cys Thr Ser Ala
785 790 795 800

Thr Met Ser Ala Val Thr Ala Pro Ala Val Glu Ala Thr Ala Glu Gly
805 810 815

Lys Val Pro Met Val Ala Thr Pro Val Gly Pro Met Pro Gly Ile Leu
820 825 830

Ile Leu Arg Gln Asn Lys Lys Pro Ala Lys Lys Arg Asp Gln Ile Val
835 840 845

Ile Val Lys Ser Asn Val Glu Ser Lys Glu Glu Glu Ala Asn Lys Glu
850 855 860

Val Ala Val Ala Ala Glu Glu Asn Ser Asn Asn Ser Ala Asn Ser Gly
865 870 875 880

Asp Ser Ser Asn Ser Ser Ser Gly Asp Ser Gln Ala Thr Glu Ala Ala
885 890 895

Ser Glu Ser Ala Leu Asn Thr Ser Thr Gly Ser Asn Thr Ser Gly Val
900 905 910

Ser Ser Asn Ser Ser Asn Val Gly Ala Asn Thr Asp Gly Asn Asn His
915 920 925

Ala Glu Ser Lys Asn Asn Thr Glu Ser Ser Ser Asn Ser Thr Ser Asn
930 935 940

Thr Gln Ser Ala Gly Val His Met Lys Glu Gln Leu Leu Tyr Leu Ser
945 950 955 960

Lys Leu Leu Asp Phe Glu Val Asn Phe Ser Asp Tyr Pro Lys Gly Asn
965 970 975

His Asn Glu Phe Leu Thr Ile Val Thr Leu Ser Thr His Pro Pro Gln
980 985 990

Ile Cys His Gly Val Gly Lys Ser Ser Glu Glu Ser Gln Asn Asp Ala
995 1000 1005

Ala Ser Asn Ala Leu Lys Ile Leu Ser Lys Leu Gly Leu Asn Asn
1010 1015 1020

Ala Met Lys
1025

<210> 10
<211> 705
<212> PRT
<213> Caenorhabditis elegans

<400> 10

Met Gln Ala Val Phe Glu Thr Thr Leu Thr Gln Lys Met Asp Gly Val
1 5 10 15

Met Ile Val Gln Glu Thr Thr Thr Asp Leu Ala Asp Thr Leu Glu Asn

20

25

30

Ala Ser Ile Ser Ala Glu Lys Ser Glu Gln Lys Pro Glu Arg Leu His
35 40 45

Pro Gln His Trp Cys Gly Gln His Lys Phe Glu Ala Asp Ser Pro Thr
50 55 60

Asn Phe Tyr Asp Tyr Thr Asn Ala Lys Glu Lys Glu Lys Ser Ala Met
65 70 75 80

Cys Arg Val Ala Glu Ile Ala Arg Phe Asn Lys Leu Arg His Val Tyr
85 90 95

Asn Leu Gln Asp Glu Ser Gly Pro Ala His Lys Lys Leu Phe Thr Val
100 105 110

Lys Leu Val Leu Thr Glu Ala Glu Thr Phe Glu Gly Ser Gly Thr Ser
115 120 125

Ile Lys Arg Ala Gln Gln Ala Ser Ala Glu Ala Ala Leu Lys Gly Thr
130 135 140

Lys Leu Pro Leu Pro Thr Glu Lys Pro Thr Lys Lys Arg Ile Asn Asp
145 150 155 160

Thr Thr Lys Pro His Arg Val Leu Gln Asn Val Cys Arg Thr Leu Gln
165 170 175

Tyr Gln Met Pro Asn Tyr Ile Ser Cys Asn Pro Pro Val Tyr Pro Asp
180 185 190

Pro Gly Cys Pro Leu Pro Glu His Ile Leu Leu Pro Leu Glu Ser Met
195 200 205

Ala Leu Tyr Ala Pro Pro Phe Pro Thr Leu Pro Ile Asp Pro Ala Arg
210 215 220

Pro Gln Gly Pro Lys Leu Gln Ala Val Ile Val Asn Ile Asn Gly Lys
225 230 235 240

Ser Ile Ala Thr Gly Ile Gly Glu Thr Tyr Pro Leu Ala Lys Gln Asp
245 250 255

Ala Ala Ala Lys Ala Leu Ala Val Leu Ser Pro Leu Leu Arg Glu His
260 265 270

Gln Asn Gly Ser Asp Asn Gly Phe Gly Lys Glu Asn Ile Pro Val His
275 280 285

Lys Gln Lys Ser Val Ile Ser Asp Ile His Glu Lys Ala Tyr Gln Leu
290 295 300

Lys Val Asn Val Val Phe Glu Val Leu Lys Glu Glu Gly Pro Pro His
305 310 315 320

Asp Arg Gln Tyr Val Val Arg Cys Ala Phe Val Thr Ser Gly Asn Val
325 330 335

Val Lys Ala Glu Ala Val Gly Lys Gly Lys Lys Lys Lys Ser Ala Gln
340 345 350

Gln Glu Ala Cys Thr Gln Leu Leu Ala Thr Val Glu His Leu Thr Pro
355 360 365

Glu Asn Asn Pro Val Ala Leu Ala Thr Asn Val Cys Lys Thr Gln Lys
370 375 380

Lys Leu Ala Ala Met Asn Arg Glu Pro Lys Arg Lys Thr Ile Val Lys
385 390 395 400

Asp Lys Lys Met Asp Pro Leu Tyr Gly His Gln Ile Asn Pro Val Ser
405 410 415

Arg Leu Ile Gln Val Thr Gln Ala Lys Ser Lys Glu His Pro Thr Phe
420 425 430

Glu Leu Val Ala Glu His Gly Val Ser Lys Tyr Lys Glu Phe Ile Ile
435 440 445

Gln Val Lys Tyr Gly Asp Asp Val Gln Glu Gly Lys Gly Pro Asn Lys
450 455 460

Arg Leu Ala Lys Arg Ala Ala Ala Glu Ala Met Leu Glu Ser Ile Gly
465 470 475 480

Phe Val Lys Pro Leu Pro Pro Pro Gly Lys Ser Leu Leu Lys Lys Met
485 490 495

Ile Asp Cys Asp Pro Ser Leu Pro Glu Ile Ser His Trp Thr Gly Pro
500 505 510

Pro Pro Thr Ala Val Ser Val Ser Thr Ser Glu Pro Asp Thr Ser Glu
515 520 525

Ala Ala Gln Leu Ser Pro Glu Gln Thr Asp Ile Ser Glu Lys Arg Glu
530 535 540

Leu Ser Pro Asp Thr Glu Lys Arg Arg Val Thr Phe Asn Ser Gln Val
545 550 555 560

His Ala Cys Pro Pro Pro Gly Asp Gln Asp Tyr Pro Asn Ser Ile Val
565 570 575

Gln Ser Leu Lys Lys Asp Ala Ile Val Glu Gly Lys Ile Arg Arg Leu
580 585 590

Lys Arg Ser Lys Glu Asn Arg Arg Ala Leu Thr Ala Glu Gln Ile Val
595 600 605

Glu Leu Ser Glu Arg Ala Gln Ser Tyr Leu Gln Thr Lys Asn Thr Thr
610 615 620

Ile Gln Ser Ser Gln Ser Ser Ser Ala His His His Leu Glu Gln Leu
625 630 635 640

Ser Asp Phe Phe Lys Phe Ser Leu Gln Tyr Thr Ser Phe Pro Gln Val
645 650 655

Gly Ile Asp Gln His Phe Thr Ile Val Ser Ile Gly Leu Glu Ala Pro
660 665 670

Leu Val Gly His Gly Thr Gly Cys Ser Thr Thr Glu Ala Asp Glu Asn
675 680 685

Ala Ala Leu Asp Ala Ile Ala Lys Leu Lys Glu Leu Ser Ala Ser Lys
690 695 700

Thr
705

<210> 11
<211> 101
<212> PRT
<213> Homo sapiens

<400> 11

Gly Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser

1 5 10 15
 Glu Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr
 20 25 30
 Phe Phe Asp Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu
 35 40 45
 Asp Glu Phe Arg Leu Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly
 50 55 60
 Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln
 65 70 75 80
 Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys
 85 90 95
 Ala Thr Val Thr Ala
 100

<210> 12
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 12
 Lys Glu Lys Thr Lys Thr Lys Lys Pro Gly Thr Lys Thr Lys Ser Ser
 1 5 10 15
 Ser Pro Val Lys Lys Ser Asp Gly Lys Ser Lys Pro Leu Ala Ala Ser
 20 25 30
 Pro Lys Pro Ala Gly Leu Lys Glu Ser Ser Asp Lys Val Ser Arg Val
 35 40 45
 Ala Ser Pro Lys Lys Lys Glu Ser Val Glu Lys Ala Ala Lys Pro Thr
 50 55 60
 Thr Thr Pro Glu Val Lys Ala Ala Arg Gly Glu Glu Lys Asp Lys Glu
 65 70 75 80
 Thr Lys Asn Ala Ala Asn Ala Ser Ala Ser Lys Ser Ala Lys Thr Ala
 85 90 95
 Thr Ala

<210> 13
<211> 16
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 13
agcttaatta gctgac

16

<210> 14
<211> 16
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 14
agctgtcagc taatta

16

<210> 15
<211> 31
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 15
cctggatccg aaagtatagc ttctaccatt g

31

<210> 16
<211> 36
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 16
tacataagct tctagatggc cagaaaaggt tcagca

36

<210> 17
<211> 27
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 17
ggatgaatcc tattagtaga cttgcac

27

<210> 18
<211> 29
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 18
gctctagatt caaagttccc caggcgcag

29

<210> 19
<211> 29
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 19
tttaagcttc tcagagggtc tagtgcgag

29

<210> 20
<211> 22
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 20
caatgtataa gcccgtaggac cc

22

<210> 21
<211> 36
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 21
aaaaagcttg tgcaagtcta ctaataggat tcatcc

36

<210> 22
<211> 18
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 22
atagcccag agttgttg

18

<210> 23

<211> 36
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 23
 tacataagct tctagatggc cagaaaaggt tcagca 36

<210> 24
 <211> 29
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 24
 tacatgtcga cttcctgccc ggctgcggg 29

<210> 25
 <211> 44
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 25
 tacaatctag attatcagcg gccgcacctc ccacacacag acat 44

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 26
 tacataagct taagccacca tgggtcaaagt tccccaggcg c 41

<210> 27
 <211> 40
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 27
 tacaatctag agcggcccg ctcagagggt ctagtgcgag 40

<210> 28
 <211> 28

<212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 28
 acaggatccc ttgtgacgag gggtcggt 28

 <210> 29
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 29
 acaggatccc caaaactcct gccttatg 28

 <210> 30
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 30
 acaggatccc caaaactcct gccttatg 28

 <210> 31
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 31
 acaggatccc aaaattccct ggccttcc 28

 <210> 32
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 32
 acaggatccc ttgtgacgag gggtcggt 28

 <210> 33
 <211> 28
 <212> DNA

<213> Artificial
 <220>
 <223> oligonucleotide
 <400> 33
 acaggatccc gtaatttttg ctgacctg 28
 <210> 34
 <211> 28
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide
 <400> 34
 acaggatccc aaaattccct ggccttcc 28
 <210> 35
 <211> 28
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide
 <400> 35
 acaggatccc attagcctgt ctctcagt 28
 <210> 36
 <211> 28
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide
 <400> 36
 acaggatccc ttgtgacgag gggtcgtt 28
 <210> 37
 <211> 28
 <212> DNA
 <213> Artificial
 <220>
 <223> oligonucleotide
 <400> 37
 acaggtacca tgggtgcgag agcgtcag 28
 <210> 38
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> oligonucleotide

 <400> 38
 acaggtacca tgggtgcgag agcgtcag 28

 <210> 39
 <211> 29
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 39
 acaggtacca tgcctatagt gcagaacat 29

 <210> 40
 <211> 29
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 40
 acaggtacca tgcctatagt gcagaacat 29

 <210> 41
 <211> 29
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 41
 acaggtacca tgcctatagt gcagaacat 29

 <210> 42
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <223> oligonucleotide

 <400> 42
 acaggtacca tgggtgcgag agcgtcag 28

 <210> 43
 <211> 28
 <212> DNA
 <213> Artificial

<220>
<223> oligonucleotide

<400> 43
acaggtacca tggctgaagc aatgagcc 28

<210> 44
<211> 28
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 44
acaggtacca tgcagagagg caatttta 28

<210> 45
<211> 28
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 45
acaggtacca tgcttcagag cagaccag 28

<210> 46
<211> 30
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 46
gatgctcgag atgaaacttg gaaaaaaacc 30

<210> 47
<211> 41
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 47
cacatctaga tcattttattc agcggccgca ctgagcagcg t 41

<210> 48
<211> 22
<212> DNA
<213> Artificial

<220>

<223> oligonucleotide

<400> 48

ctgagcctgg gagctctctg gc

22

<210> 49

<211> 42

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide

<400> 49

tccagtgatt tttttctcca tgcttgccca tactatatgt tt

42

<210> 50

<211> 23

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide

<400> 50

tcattgccac tgtcttctgc tct

23

<210> 51

<211> 21

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide

<400> 51

ccgcagatcg tcccagataa g

21

<210> 52

<211> 21

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide

<400> 52

aaatagcaca gtttgcaaac t

21

<210> 53

<211> 21

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide

<400> 53
aattctccga acgtgtcacg t 21

<210> 54
<211> 20
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 54
tttaccaggg cagctccgaa 20

<210> 55
<211> 26
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide

<400> 55
caactcagac agcaacttta agatgt 26

<210> 56
<211> 575
<212> DNA
<213> Artificial

<220>
<223> unknown

<220>
<221> promoter
<222> (1)..(503)
<223> U6 promoter

<220>
<221> misc_feature
<222> (221)..(221)
<223> n is a, c, g, t or u

<220>
<221> misc_signal
<222> (504)..(504)
<223> G = transcription initiation signal

<220>
<221> misc_RNA
<222> (505)..(532)
<223> antisense region of stauken siRNA

<220>
<221> misc_feature
<222> (533)..(540)

<223> linker

<220>

<221> misc_RNA

<222> (541)..(568)

<223> sense region of stauflen siRNA

<220>

<221> misc_signal

<222> (569)..(575)

<223> transcription termination signal

<400> 56

```
aagcttggct gcaggtcgac ggatcccccc gagtccaaca cccgtgggaa tcccatgggc      60
accatggccc ctcgctccaa aaatgctttc gcgtcgcgca gacactgctc ggtagtttcg      120
gggatcagcg tttgagtaag agcccgcgtc tgaaccctcc gcgccgcccc ggccccagtg      180
gaaagacgcg caggcaaaac gcaccacgtg acggagcggtg nacccgccga gcgcgcgcca      240
aggtcggggca ggaagagggc ctatttccca tgattccttc atatttgcac atacgatata      300
aggctgttag agagataatt agaattaatt tgactgtaaa cacaagata ttagtacaaa      360
atacgtgacg tagaaagtaa taatttcttg ggtagtttgc msycttaaaa ttatgtttta      420
aatggacta tcatatgctt accgtaactt gaaagtattt cgatttcttg gctttatata      480
tcttgtggaa aggacgaaac accgtaaggg tcaacaggct tatacattgg ttgaagcttg      540
agccgatgta taagcctggt gatccttatt tttttt                                575
```